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length: 2000000000
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KEYWORDS
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FEATURES
                                        source
                                                   Unclassified.

1 (bases 1 to 1026)
Wayne, J. and Xu, S.
Method for construction of thermus E.
Method for construction of thermus plasmid
identification of two Thermus plasmid
Patent: US 620737-A 4 27-MAR-2001;
Location/Qualifiers
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Sequence 4 from patent US 6207377.
AR139424
AR139424.1 GI:14481920
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323 c 285 g
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Thermus sp. YS45
Bacteria; Thermus/Deinococcus
1 (bases 1 to 1600)
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Direct Submission
Submitted (12-FEB-1997)
Road, Beverly, MA 01915,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wayne, J. and Xu, S.Y. I thermophilic plasmid origin Identification of a thermophilic plasmid origin within a new Thermus-E. coli shuttle vector Gene 195 (2), 321-328 (1997)
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/note="putative;
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/gene="repT"
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/product="replication protein"
/protein_id="AAB72144.1"
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KILELLQEIARSTIPYGNRELMRKVGTVVFMVPLEMLALULGYRGYTHAWKVLEKK
GLVATDVLHQTVNGERRAIGTLMAVRLRPGKRALTLDDYIPPRNLALDMANGVLSFN
WVKAYQDHGIRFTLDVLVLWAQGKRVMENTKTVAVDLGLILVLPEVERSKLPALITLI
ATYIADLLDDRRSRRFFYAGLLMAVARGELPAQYLFAVLMRVIRDYTDGHLTRPGAYLV
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243. .2
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                                                                                          Wayne, J. and Xu,S. Y.
Method for construction of thermus-E.
identification of two Thermus plasmid
patent: US 6207377-A 6 27-MAR-2001;
Location/Qualifiers
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Streptomyces
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                  coelicolor cosmid
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30S ribosomal protein S2; 50S ribosomal protein L19; cell division protein FtsH homolog; elongation factor Ts; ffh; ftsH; glnB; glnD; nitrogen regulatory protein pII; prophage; protein pII uridylyltransferase; pyrH; RNA polymerase sigma factor WhiG; rpbS; rpsB; rpsP; signal peptidase I; signal recognition particle protein; sip1; sip2; sip3; sip4; trmD; tRNA (guanine-N1)-methyltransferase; tsf; uridylate kinase; whiG. streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-JUN-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
3 (bases 1 to 38962)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 mb Streptomyces coelicolor A3(2) chromosome
mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Generally where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Streptomycineae; 1 (bases 1 to 38962)
                                                                                                                                                                                                                                                                                                                                    jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                        prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Framerlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notes: Streptomyces coelicolor sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                   IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 2E1 lies between 7A1 and 6A9 on the AseI-B genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are also included but some of these may be fortuitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the BBSRC.
                                                                                                                                                                                                                                                                                                                      upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.nih.go.jp/
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                                       /gene="glnB"
<1. .166
                                                                                                                     /strain="A3(2)"
/db_xref="taxon:100226"
  /gene="glnB"
/note="SC2E1.
                                                                                                                                                                                                Location/Qualifiers
                                                                                                   /clone="cosmid
                                                                                                                                                             organism="Streptomyces"
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  ginB,
      nitrogen
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Streptomycetaceae; Streptomyces
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                             TEANS LATION - "MIVRSVORAGILCLEGRIPWRITH NADARTYAAVEDILSDRLS
ATFKSLEGKGRLTEADIDATAREITIALLEADVALPVVRAFIKKYERSLEAREVSKAL
NPAQOVLKI VENEELVGILIGGETRIKERFAKOPPTVINLAGLOGAGKTILAGKLGHWLKE
GGHSPLLVACDLORPNAVNQLSVVAERRGVAVVAPECGNGVGDPVKVAKDSIEFAKAK
VHDLVIVDIAGRLGIOQELMQQAADIRDAVSPDEILFVVDAMIGQDAVNTAEAFRDGV
GFDVVLSKLDGDARGGAALS ISVITGK NASNGEKUDPURDAVEQURKNGSRILDMG
DLLTILEQAEKTFSQEEAEKMASKLASKKGQDETLDDFLAQMEQVRKNGSISKLIGML
PGMGQMKDQINNLDERDVDRTAAIIKSMTPGERQEPTIINGSRRARIAKGSGVEVSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"SC2E1.03, ffh, signal recognition particle protein, len: 550 aa; highly similar to mmay e.g. SR4_ECOLI (453 aa), fatsa scores: opt: 1465 z-score: 1282.8 E(): 0, 50.08 identity in 458 aa overlap. Contains PS00017 ATP/GTP-binding site motif A (P-loop), PS00300 SRP54-type proteins GTP-binding domain signature and Pfam match to entry SRP54 PF00448, SRP54-type proteins, score 66.57. Similarities suggest possible start site at aa 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLFGAATEEHTGISLVAVGGYGGELSPRSDLDLLLLIADGRDKAVAALADRLWYPW
DLGIDLDHSVRTPOQARKTAGODLKVHLGLLDARHLAGDLGITASLATAVAADWRNQA
PKRLPELRDLCAERAEROGELQFLLEPDLKEARGGLRDATALRAVAASWLADAPREGL
AEARRRLLDVRDALHLATGRATTDRLALQEQDQVAAELGLLDADALLRQVYEAARVIS
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RPDLLLIAALLHDIGKGWPGDHSVAGETIARDVAARIGFDGADTAVLATLVRHHLLLY
ETATRROLDDPATVRAVAQAVGTEHTLELHALTEADALATGPDAAWSSWRGSLVADLV
KNLVERFFEARKMMSRMAQGGGMPGMPGMPGMGGGPGRQKKQQKKAKGKQRSGNPMKF
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SSPSFSPSADGPEPLGVELLTAVEGGVLAVAGVLAWARLTVRFYAEL
RSVPLPDGVESSYLLLDAWRVAAGVSGLPQAARLRADLVRALDGTLDIAARLABEDAAL
PRRRGYEPPEPRVTVAPAASRLATVLEVRAQDAPGLLFRLGRALEAAGVRVRSAHVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       partial CDS, len: >54 aa; highly similar to many e.g. GLNB_AZOBR (112 aa), fasta scores; opt: 198 z-score: E(): 4.9e-14, 50.0% identity in 54 aa overlap"
                                                                                                                                                                                                                                                                                                                         /db_xref="GI:3191979"
/db_xref="SPTREMBL:069874"
                                                                                                                                                                                                                                                                                                                                                                                               /product="signal recognition
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/protein_id="CAA19377.1"
/db_xref="GI:3191978"
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/protein_id="CAA19376.1"
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Local Similarity 46.3%;
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                                                          CCGCGCTGCTGCACGACATCGGCCAAAGGCTGGCCCGGCGACCACTCCGTGGCCGGCGAGA 1662
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/product="Cell division protein FtsH homolog"
/protein_id="CaAl9379.1"
/db_xref="Gi:3191980"
/db_xref="SPTREMBL:069875"
/translation="MTNPSPPRKAPEPPWRTEGTPDEPPKPPPGGRRMRGGWMNLILA
/translation="MTNPSPPRKAPEPPWRTEGTPDEPTSYTEPSKOVDEGNYSKIYAKGDAIOGOLKKARDNP-
EGDGTYTKTTERPTFADDQLWADLIKNRVTVTAEPVVQHRSFLANLLIALAPMLILV
VLMIFIARNIGALGGGAGGMLGRKAPPKPUELEAGKPRTTFADVAGIDEVEGELSDV
VDFLKUNDAYTRMGALGGAGGMLGRKAPPKPUELEAGKPRTTFADVAGIDEVEGELSDV
VDFLKUNDAYTRMGAKMPRGVLLTGPPGTGKTLLARAVAGEAGVPFESAAASEFIEMI
VGVGASRVREDFABARKVAPSIFIDEIDTIGRARGGGGGGHDEREQTLNQILTEM
DGFSGSEGVIVIAATNRADILDAALTRPGRFDXVSVSPDRGGREAILEIHTREIPL
APDIDLAQVARTTPGMTGAELANLANDAALLAVKRKODRVTQANLESALEKVQLGAER
PLVMPEEEERRTAYHESGHALLGMLOPGADPVRKITIYPRGRALGVTLSTPDADKYAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3566. .3697
/gene="ffh"
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ALPGDAQQAYGLAAAPQTLDAIDGEMRRVVDSCYEEAVRKLRDHRGQLDALAESLLAS
ETLDEADAYRIAGITRLTKDDPEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 various cellular activities (AAA) and to entry zn-protease PF00099, Zinc-binding metalloprotease domain, score 22.07, score 357 96. Proline-rich N-terminus is not present in other ftsH homologs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry AAA PF00004, ATPases associated with various cellular activities (AAA), score 357.96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"hairpin loop with 22/23 bp stem" 4504..6450
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/transl_table=11
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proteins, score 66.57"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane protein; phosphate binding protein; regulatory protein; secreted beta-galactosidase; secreted protein. Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2) Bacteria; Firminosto. A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Notes:
Streptonyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-MAY-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCC42
Streptomyces coelicolor
AL356992
                                                                                                                                                                                                                                            The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at hit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown, S.P. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach, M., Kieser, H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
correct initiation codon. Where possible we choose an initiatic codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the n
                                                                                                                           jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand)
                                                                                                                                                                                                                     http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 13347)
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cosmid C42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCT
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IMPORMANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.

Cosmid C42 Overlaps with cosmid C24 on the AseI-C.
                                                    /gene="SCC44.ou"
/gene="SCC42.03c"
/gene="SCC42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(493..1257)

/gene="SCC42.02c"
/gene="SCC42.02c"
/note="SCC42.02c, possible ABC-transporter integral
/note="SCC42.02c, possible ABC-transporter integral
membrane protein, len: 254 aa; similar to TR:053546
(EMBL.AL022022) Mycobacterium tuberculosis hypothetical
(EMBL.AL022022) Mycobacterium tuberculosis hypothetical
26.6 kD protein MTV023.08c, 254 aa; fasta scores: opt: 88
z-score: 1004.0 E(): 0; 50.8% identity in 242 aa overlap.
Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="SCC42.01c, possible ABC-transporter integral membrane protein (fragment), len: >161 aa; similar to membrane protein (fragment), contains tuberculosis through the state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(491..494) complement(493..1257)
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fgsgglgviggtigvmiamtlftgtvvgiqgyaaldqigtsaftgfvsayfntreiap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein (fragment)"
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/strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MITGALROTGRLFALAAEVVRAVFRRPFQFRFYEQFWYVASVT
ILPAALVSIPFGAVIALQVGSLTEQLGAQSFTGGASVLAVVQQASLIVALLIAGAGG
SAICADLGSRRIREELDAMEYMGVSEVQRLLVPRVLAAMGVAVLLNGLVSVVGILGSV
FENVIMQGGTPGAYLSSFSALAQLPDLYVSELKALVFGFIAGIVAAYRGLNPRGGPKG
VGDAVNQSVVITELLLFFVNNYMTAVYLQIVPPKGG"
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/db_xref="GI:8247036"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB92895.1"
/db_xref="GI:8247037"
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/transl_table=11
    /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                         /product="putalive secreted protein"
/product="putalive secreted protein"
/protein_id="CAB92898.1"
/db_xref="gi:8247040"
/db_xref="gi:8247040"
/translation="MKATPAAAPRPSRARATTSIAAFVVLAALVPTTASASGTQEVE
AELPYVCTLPSGQLPATVRVSAEPPERAGADEAFTPSDVTTTVELPAEAVADLTARDA
AEVRANTSIAAVVAQNTATAAVTWRGSAEPVALPSGGPLTLVTTGDVPSYAGRSDGDL
TESAGALAIDLALGAADPATADPGSLTVUCTLAEDAPGQGLLATVPVGTDGQAFSGSSP
SSGGPAGSSGAPDDDGRQDGPGDRREERQSERSPKVLENTPGAAADRDDVPPCRVDEQ
PSTDVSLNAVTGYANVKKMKGAAYLPPSCVLIEQGLPVFGPDDFYXLIFDTLSYAN
FHYRERKQTPPFEATFLSFDFAPVKATMVLEQTGTMRIDSRMKIRLSDFTITDTYVR
APLVLHVLDLEVNGTPLDVGSECRTETSLTSEDPDAMFPGDHLVLYGRGEQLIGLPA
TGYLLLSGGALSGAATIPAFTGCGSDEDLDRLTTASVSGPGNYIKQVQGQTCAIAAP
VFPSFENEGQCTEDLQPYEIFVAER"
5323..6264
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transporter, score 152.90, E-value
complement(1800. .1844)
/gene="SCC42.03c"
/note="PS00211 ABC transporters famous famou
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/note="PS00017 /
2904. .2909
                                                                                                   sequence"
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/note="SCC42.05"
/note="SCC42.05, possible secreted protein, len: 533
Contains possible N-terminal region signal peptide
sequence. High content in alamine amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCC42.05"
3687. .5288
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avnvgnivltatipmtcttstaagtmasatgnpgdvadittmnpgasgspctsvlgnv
tttsvtpwdvvgvdynsstgvtkgyvgnvkanvtagackftvtgkasgtytnstgvla
instagelavsnpvncgaivttatkptfkgnvavtvastgaiptivgsnp"
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3687. .5288
/product="putative secreted
                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                         /gene="SCC42.06"
/note="SCC42.06,
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/protein_id="CAB92897.1"
/db_xref="GI:8247039"
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/note="SCC42.04, |
Contains possible
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/gene="SCC42.04"
2918. .3550
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/protein_id="CAB92896.1"
/db_xref="GI:8247038"
/translation="MASAGGDMGIEVVVEGLTKSFGKQSIWRDVSLTLPAGEVSVMLG
PSGTGKTVFLKSLIGLLKPEKGRVLINGVDMVNSPERDIYETRKLFGLMFQDGALFGS
MSLFDNIAFPLREHTEKKESEIRRIVMERIEVVGLLGAEGKLPGEISGGMRKRAGLAR
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/gene="SCC42.03c"
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GMLFLRQLVTFGPREVLLTSDEPVVAQFLGGRREGPIGMSEEKDAATLAAEADAAPAA
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complement/1777
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PMPAAGSGA"
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Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL391406.1 GI:9857143
AbaA-like; AraC-family; ATP/GTP-binding membrane; bldA;
AbaA-like; AraC-family transcriptional regulator; hydrolase;
DNA-binding; GntR-family transcriptional regulator; hydrolase;
integral; integrase; MarR-family; NLP/P60-family secreted; pgm
phosphoglycerate mutase; TetR-family; transferase; transport.
Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                      Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                       3 (bases 1 to 35576)
Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                    2 (bases 1 to 35576)
Brown, S.P. and Harris, D.
                                                                                                     Colney, Norwich, Norfolk NR4
                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Streptomycineae; Streptologic loases 1 to 35576)
Redenbach, M., Kieser, H.M., Denapaite, D.,
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Streptomyces coelicolor
AL391406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid 2D46 lies between and overlaps cosmids D66 and D8 on the AseI-D genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Mucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coelicolor),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (URL; http://www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          more significant matches with motifs in the PROSITE database
/note="2SCD46.02, possible GntR-family transcriptional regulator, len: 303aa; similar to many eg. TR:Q9RIQ2 (EMBL:AJV43257) KORA protein from plasmid pSNA1 of Streptomyces natalensis (245 aa) fasta scores; opt: 175, z-score: 204.2, E(): 0.00069, 28.2% identity in 238 aa overlap. Also strongly similar to neighbouring CDS 2SCD46.04 fasta scores; opt: 1074, z-score: 984.2, E(): 0.7.6% identity in 302 aa overlap. Contains Pfam match to entry PF00392 gntR, Bacterial regulatory proteins, gntR family and helix-turn-helix motif (Score 1967 (+5.89 SD))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="2SCD46.01c"
/note="2SCD46.01c, unknown, partial CDS, len: >45aa;
/note="2SCD46.01c, unknown, partial CDS, len: >45aa;
strongly similar to neighbouring CDS 2SCD46.03c fasta
scores; opt: 169, z-score: 236.7, E(): 1.4e-07, 51.1%
identity in 45 aa overlap. Hydrophobic."
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="2SCD46.02"
289. .1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(142. .147)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Nominal overlap with Streptomyces coelicolor cosmid
D66 (EMBL:AL358692)"
                                                                                                                                                                                                                                                                                                                               /gene="2SCD46.02"
/note="2SCD46.02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="CACO4023.1"
/db_xref="GI:9857144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Repeated degenerately at 1210...2414. This DNA repeat manifests as a duplication of a pairs of CDss such that 2SCD46.01c is similar to 2SCD46.03c and 2SCD46.02 is similar to 2SCD46.04."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MPLIAIVVAALAIGFEQLVQWKYGPMGIIAFVALSIGIKAKNTMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="cosmid 2D46"
complement(1. .135)
/gene="2SCD46.01c"
1. .1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism≈"Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .sanger.ac.uk/Projects/S_coelicolor/)
using the following system eg SC7B7.01c. SC (S.
(cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .135)
                                                                  gene
   CDS
                                                                                                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_unit
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/note="2SCD46.04, possible GntR-family transcriptional regulator, len: 291aa; similar to many eg. TR:09RIQ2 (EMBL:AJ424257) KorA protein from plasmid pSNA1 of Streptomyces natalensis (245 aa) fasta scores; opt: 175, z-score: 209.9, E(): 0.00033, 29.9% identity in 194 aa overlap. Also strongly similar to neighbouring CDS 2SCD46.02 fasta scores; opt: 1074, z-score: 984.2, E(): 0, 57.6% identity in 302 aa overlap. Contains Pfam match to entry pPG0392 gntR. Bacterial regulatory proteins, gntR family and helix-turn-helix motif (Score 2173 (+6.59 SD)) at residue 41-62. Note possible alternative downstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="2SCD46.04"
1539. .2414
                                                                                    regulatory proteins, 7.2e-20"
                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product="putative GntR-family transcriptional regulator"
/protein_id="CAC04026.1"
/db_xref="GI:9857147"
/gene="2SCD46.05"
2363. .3184
                                                                                                                                                                                                                                                             LNGEEALLGYYMLTRREEEYESRTLQMYDALGSQSLLFSFLNRTGHRDAVFVEESQKW
                                                                                                                                                                                                                                                                                                 VLVEDEEDDPVHQRWLQMRNAQARVLQHNLHAVRSTHRVDVRIAFRALPFTPPMKLYI
                                                                                                                                                                                                                                                                                                                    ELAEEFGVERGTVRQALRĀLQEDGLLTNVSKGSPPRIAEPATPRAEPQPTMVALGPRL
AEAFAAPHVRVDVVCHTSETLMLALSEPLRLIHEGRIHPESIDFRVLMPSRDIALAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Repeated degenerately at 1210...2414. This DNA repeat manifests as a duplication of a pairs of CDSs such that 2SCD46.01c is similar to 2SCD46.02 and 2SCD46.02 is similar to 2SCD46.04."
                                                                                                                                                                                                                                                                                                                                                                                  translation="MVVTQENVSVNGSRRLSSQEIADVLRERIRGGDLRAGDRLPTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translational start codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1210. .1398)

/gene="25CD46.03c"
/note="25CD46.03c, unknown, len: 62aa; strongly similal neighbouring CDS 25CD46.03c fasta scores; opt: 169, z-score: 236.7, E(): 1.4e-07, 51.1% identity in 45 aa overlap. Hydrophobic."
                                                                                                                                                  note="Pfam match to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="2SCD46.04"
/note="2SCD46.04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="CAC04025.1"
/db_xref="GI:9857146"
/translation="MPVLALVSAVFVIAFEQIVQWRYGATGIVGLLLLTIGIKAKSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPTQAQLAEEFGVERGAVRQALRILQSERLLTNVSKGSPATVAPDPYGPQSGPEARPM
PTTVALASRIAAAFAAEHVEIDALCLTSVSLTLALGEPLSQIHAGRLKPAKVDVRVLL
PSGDIDLAFPVAVSGCAAGGPVHERWLAMRNAQGQVLRHNLLSLRATHGIDVRVSFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSSAGAVLLALLVAGPAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGVFVKQSRLWFDALWGTISSELVLAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPFTPPVKLYVLNGSEALFAYYTLGRREQEIDHEQLEMYDAEGIRSTLFAFEQGGGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative GntR-family transcriptional regulator"
/protein_id="CAC04024.1"
/db_xref="GI:9857145"
/translation="MYVEPEHAPVNGRERPORPQATHREVADELRARIRSGRLRPGOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at residue 46-67. Note possible alternative downstream translational start codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="2SCD46.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Pfam match to entry PF00392 gntR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                    .3184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1398)
                                                                                                                 gntR family, score 69.30, E-value
                                                                                                                                               entry PF00392 gntR, Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       len: 62aa; strongly similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 64.70, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial
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DEFINITION
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Best Local S
                                                                                                                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 174;
  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 tggccctcaacctgggggtcacccggcagaccgtccacgcctggaagaaggtccttgaga 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
In ALI18514

NALI18514

ALI18514

ALI18514

ABC transport protein, ATP-binding subunit;

amidophosphoribosyltransferase; ATP-dependent helicase;
amidophosphoribosyltransferase; DNA polymerase III subunit gamma;
ATP-dependent RNA helicase; DNA polymerase III subunit gamma;
DNA-binding protein; integral membrane protein; lipoprotein;
LSR2-like protein; luxR family; phosphoribosyl formylglycinamidine
synthase II; phosphoribosylamine-glycine ligase;
phosphoribosylaminoimidazole-succinocarboxamide synthase;
phosphoribosylformylglycinamidine cyclo-ligase;
phosphoribosylformylglycinamidine cyclo-ligase;
phosphoribosylformylglycinamidine synthase I; secreted peptidase;
sensor kinase; transposase; tRNA; two-component transcriptional
regulator; valine dehydrogenase.
Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toggcaccctttgggccgtccggctgaggccagggaaagccaggctcacccttggacgact 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTCACCCGGCCACCACCGCCCTCCCGCCCGTCGAACTGGCCCCCGGCGTCC 16427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaaagggcctggtggccaccgacgtccttcaccaaaaccgtcaacggggagcgccgggcca 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAACGTCTACATCGTGGAGCTGGCGCAGCGCCTCGCCGCGATCAACATCGAGGTCGAGA 16367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGGGGCGCGCCCTGGTGCACGCCATGCACCATGGCCAAGGTCAAGAACGCCAACC 16667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctcaggggaaaagggtgatgcccaacaccaagaccgtggccgttgacctgggcctcatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gggtcaaggcotaccaggaccacggaatccgccccaccctggacgtgctggtcctctggg 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTCTGCGCCTTCACCCACGGCGTGATGCAGGCCTGGGCCGGTCACCGCCCCGGCCACT 16547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acatctacccctggaggaacctcgccctagacatggccaacggcgtgctctccttcaact 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCCGACGGCGA 16680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tggtcctccccga 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/note="2SCD46.05, possible hydrolase, len: 273aa; weakly /note="2SCD46.05, possible hydrolase, len: 273aa; weakly similar to many proposed phosphatases eg. TR:CAB84916 (EMBL:AL162756) putative phosphatase from Neisseria meningitidis (235 aa) fasta scores; opt: 195, z-score: 238.2, E(): 8.8e-06, 29.5% identity in 237 aa overlap. Contains Pfam match to entry PP00702 Hydrolase, haloacid dehalogenase-like hydrolase. Note possible alternative downstream translational start codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"putative hydrolase"
/product-"putative hydrolase"
/product-"putative hydrolase"
/protecin_id-"CAc04027.1"
/db_xref-"gi:9857148"
/db_xref-"gi:9857148"
/translation-"MVRRPLGNHHHGHDTLLVTSDTDOTEPVSERTGRDEQSEALRDL
/VGARYVLWDEPOGPICRLFAGYSADRVAGEL/VDWLERLGLKELLTQEEGVHPDPHVLL
VGARYVLWDEPOGPICRLFAGYSADRVAGEL/VDWLERLGLKELLTQEEGVHPDHVLL
AAVDRRHRRSDLVAEFEERLTREELRAPFTAWPTAYADALIRTWSALGYGLAVTTUNG
ARVSEYLETROLLGCRAPHIYGRTGDPHLLKDDPHCLNRALSAMGAAPARALMVGDS
RRVVSEYLETROLLGCRAPHIYGRTGDPHLLKDDPHCLNRALSAMGAAPARALMVGDS
ASDVTAARRAGVPFLGYGHNERKTKLLKQAGADTVVDSLEPVLRLLWENGTPAPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
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submitted (20-SEP-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenact, A., Market Medenacti, A., and Hopwood, D.A.

Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Microbiol. 21(1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 41622)
Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by the BBSRC and Beowulf Genomics

Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)

CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jun/cgi bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the mesupstream initiation codon. On the entire insert of the IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlaps between neighbouring submissions.

Cosmid D25 Overlaps with cosmid D17 on the AseI-D genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomson, N.R.,
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                                                                                                                                                                              /note-"SCD23.01c possible transposase, partial CDS, len: > 150 aa. Similar to many e.g. Methylobacterium sp TR:Q50409 (EMBL; X96995) transposase IS1357 (411 aa), fasta scores opt: 239 z-score: 312.5 E(): 4.7e-10 38.2% identity in 131 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCD25.01c"
complemen+//
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/gene="SCD25.01c"
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/db_xref="taxon:100226"
/clone="cosmid D25"
/product="putative transposase"
/protein_id="CAB56345.1"
/db_xref="GI:5918467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Streptomyces
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                                                                                                              transl_table=11/
                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coelicolor A3(2)"
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(phosphoribosylglycinamide synthetase) MTCY369.17 (422 aa), fasta scores opt: 957 z-score: 1033.0 E(): 0 58.3% identity in 424 aa overlap. Contains a P800184 Phosphoribosylglycinamide synthetase signature and a Pfam match to entry PF01071 GARS, Phosphoribosylglycinamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD I VNEGLTEMRGÄHSPRLÖLEL I CARVMLPAAYGDERSVMARLDR I BROVOTSGGA
GAPAMG VPGEBAHAGAGAAAP VAAPVPGGGPAARAAVRGGGAGT PPGGDESADVAA
GAPGAGAGAGTEPGABDAGGAPGGGHPQAAPS SADVAPVPAPPSPRTPSAPAAPAPAPA
SAPGAWPSAAPAGGGRRPGGWPTATPAGGGQPRTPAAPASGPAATAAQAPAAPAPA
PVSPBSGASGVDPRSLMPNILEAVKNRRRTTWILLSONAQVPGCBGTSLØLGEVNAGA
RDNTVSSGSEDVLRØALAEØFNVØWKIDAVVDPSGGAPAAGPAGPSGPSGLØLGGVAGA
RDNTVSSGSEDVLRØALAEØFNVØWKIDAVVDPSGGAPAGPSGPSGPSGLGLGSGG
GGFGGGSAGAGGTGGGGGAPAQRESASASTPAAPPQAPASAPAPAPARPRPSAPE
PPPVSPEDDITEDDDPDLDESALSGKELLVRELGATVVEEITNE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="DNA polymerase III subunit gamma"
/protein_id="CAB55347.1"
/protein_id="CAB55347.1"
/db_xref="GCI:5918469"
/translation="MSSLALYRRYRPESFAEVIGQGHVTDPLQGALRNNRVNHAYLFS
/translation="MSSLALYRRYRPESFAEVIGQGHVTDPLQGALRNNRVNHAYLFS
GPRGCGKTTSARILARCLNCEGGPTFPPCGECQSCRDLARNGFGSIDVIEIDAASHGG
                                                                                                                                                                                             /note="SCD25.04. phosphoribosylamine-glycine ligase (EC 6.3.4.13), len: 416 aa. Highly similar to many e.g. Mycobacterium tuberculosis SW:PURZ_MYCTU (EMBL; Z80226) phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (glycinamide ribonucleotide synthetase)
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PEKVIGTIRSRTHYPERLVPPEGTLRDYLAEVGGREGIAVEEGYLPLVVRAGAGSVRD
SMSVMDQLLAGAGADGVYDMTTSLLGYTDGSLLDSVVESFVSGDGSAAFGVUDHVI
GGHDERRFYTDLLEELRDLVILAAVPDAAEKGLIDAPADVVERMQEQARSFGAAELSR
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TPLWVAKDRTASLIDRAPWARVDDMPWKDIADGKEMVIRGGYHLLEVWKCVPSSERHC
LVSDGASHCGDIHADWEVPALCLPQRRPVHIEDLVLQSATGESVPVYVPNRGNSRIGR
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/product="tRNA-Ser"
1826. _4180
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                                                                                                                                                                                                                                                                                                                                                       /gene="purD"
/note="SCD25.04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PS00017
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/transl_table=11
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PVRGLDQSTGGFTLPHARQALSRPDANHHCGTCRRLRRAGLSAVGAGPSSTGASRKLR
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/protein_id="CAB56346.1"
/db_xref="G1:5918468"
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/note="SCD25.02,
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                                                                                                                                                                                                                                                                                                                    accgtcaacggggagcgccgggccatcggcaccctttgggccgtccggctgaggccagg
 CTCCCGCAAGGGCCGCACCATCATCTTCGTCCGCACCCAGCTGG
                                                                        GTCGCACCACATCCTGGTCGTGAAGCCCAAGGACAAGGCGCCGGTCACCGCGGCCATCGC
                                                                                                  caccctggacgtgctggtcctctgggctcaggggaaaagggtgatgcccaacaccaagac 749
                                                                                                                                               GTACCTGAAGGACCCGGCCTCCACGAGGTCGACGCCCCAGGGTGCCGTGACGACCAT
                                                                                                                                                                                                                        CGGCCAGCGGATGCTGTTCTCCGCCACCATGGAGAACGAGATCAAGACCCTCGTCGACCG 39563
                                                                                                                                                                                                                                                                                                                                                                         CAACCGCGGCGCCTGCTCCCTGGAGAACGTGCAGATCGCGGTCCTCGACGAGGCCGACCA 39443
                                                                                                                                                                                                                                                                                                 ccacgcctggaagaaggtccttgagaaaaagggcctggttggccaccgacgtccttcacca 509
                                 cgtggccgttgacctgggcctcatcctggtcctccccgaggtgg
                                                                                                                                                                                                                                                           gaaagccaggctcaccctggacgactacatctacccctggaggaacctcgccctagacat 629
                                                                                                                                                                                  ggccaacggcgtgctctccttcaactgggtcaaggcctaccaggaccacggaatccgccc 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SCD25.05, possible integral membrane protein, 664 as. Contains a degenerate direct repeat region: residues 469_ PYADDEA P HAPYADDEA L HYPDADDEA P HAPYAD_502. Also contains possible membrane spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCD25.05"
5857. .7851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AARAHANACDRVVVEEFLDGPEVSLFAVTDGENVRPLQPAQDFKRALDGDEGPNTGGM
GAYSPLPWADPKLVDEVVQSVLQPTVDEMRRRGTPFSGLLYAGLAITSRGVRVIEFNA
RFGDPETQVVLARLKTPLAGLLMAAATGNLADLEPLRWSDEAAVTVVVASHNYPGTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mkvlvigggarehalcrslsldpdytalhcapgnagiaevaelh
QVDALDGAAVTALAGRLGAELVVVGPEAPLVAGVADAVREAGIPVFGPSGEAARLEGS
KAFAKDVMACAGVPTARSYVCTNPAEVDAALAAFGAPYVVKDDGLAAGKGVVVTDDVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residues 469_ PYADDEA P HA HAPYAD_502. Also contains hydrophobic domains."
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5857. .78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative integral membrane
/protein_id="CAB56349.1"
/db_xref="GI:5918471"
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/gene="SCD25.05"
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/db_xref="GI:5918470"
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Best Local Similarity
Matches 127; Conserv
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    GGGCGAGGTG 88765
                                       ccccgaggtg
                                                                                   CAAGCAGCAGATCGCCAAGAACTCCACCCACGACGACGACCACCACCACCACCTCGTCCTCCA 88755
                                                                                                                       gaaaagggtgatgcccaacaccaagaccgtggccgttgacctgggcctcatcctggtcct 782
                                                                                                                                                                     GACCGTCCACGGCAACAAGTTCAGGTTCCGCGTCGAGCCCGGCCGCACCGTCGGCTACGT 88695
                                                                                                                                                                                             ggcctaccaggaccacggaatccgcccaccctggacgtgctggtcctctgggctcaggg 722
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PROGRESS ***, 2 ordered F
AC105260
AC105260.1 GI:17985870
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sumitted (28-DEC-2001) Institute of Botany, Academia Sinica, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan The nucleotide sequence of this BAC clone was generated by combining Monsanto and ASPGC-Taiwan sequencing data.

**NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of side of the pieces is believed to be correct as given, however the sizes for the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chow,T.-Y., Hsing,Y.-İ.C., Chen,C.-S., Chen,H.-H., Wu,H.-P., Liu,S.-M., Chao,Y.-T., Chang,S.-J., Chen,T.-R., Chen,Y.-L., Chow,M.-H.J., Hong,Y.-C., Hsiung,J.-N., Hsu,C.-H., Huang,J.-J., Kau,P.-I., Lee,M.-C., Leu,H.-L., Lin,S.-J., Wu,L.-F. and Shaw,J.-F. Oryza sativa BAC OJ1115D04 genomic sequence
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Oryza sativa
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1 39588: contig of 39588 bp in length 39589 39608: gap of unknown length 39609 100772: contig of 61164 bp in length.
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ow,T.-Y. and Hsing,Y.-I.C.
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milarity 50.8%;
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/db_xref="taxon:4530"
/chromosome="5"
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Pred. No. 2.9;
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                                                                                                                                                                                                                                                                    Db 166616 CCATCGCCTACGGCATCGACAAGAAGGGCGCCGAGAAGAACGTCCTCGTCTTCGACCTCG 166557
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les 212; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcaaccgggagctctggaggaaggtggggacggtcgtcttcatggtccccctggagatgt 415
gggctcaggggaaaagggtgatgcccaacaccaagaccgtggccgttgacctgggcctca 772
                                                                                       CCACCAACGGCGACACCCACCTCGGCGGCGAGGACTTCGACCAACGCCTCATGGACCACT
                                                                                                                                                                                 GCGGCGGCACGTTCGACGTCAGCATCCTCGCCATCGACAACGGCGTGTTCGAGGTCCTTG 166497
                                                                                                                                                                                                                                                                                                          toggcaccetttgggccgtccggctgaggccagggaaagccaggctcacccttggacgact 595
                                                                                                                                                                                                                                                                                                                                                              ACGCCGGCGTCATCGCCGGGCTCACCGTCGACCGCATCATCAACGAGCCCACCGCCGCCG
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
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1 (bases 1 to 167049)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (cultivar:Nipponbare) DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45406
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36605 c 37338 g 47383 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4530"
/chromosome="8"
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46.3%;
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ne 8 clone P0035F08,
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Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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*** SEQUENCING IN
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SC8A2/c
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MEDLINE
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TITLE
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                                                        source
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Streptomyces coelicolor
AL445327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics

Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                            correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-OCT-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown, S.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL445327.1
                                                                                                                                                                                                                                                                                                                                                                                 http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                        IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                                                                           restriction fragment.
                                                                                                                                  small overlap between neighbouring submissions.
between and overlaps cosmids 4A7 and C42 on the
                                                                                                                                                                                                                                                                        upstream initiation codon
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/organism="Streptomyces
/strain="A3(2)"
                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:10798655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7459 bp
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                            coelicolor A3(2)"
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                                                                                                                                                                    8A2 Lies
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        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAC12793.1"
/db_xref="GI:10798657"
/db_xref="GI:10798657"
/translation="MITLAVRLAULAFILIAVLALSFLGIRYADLGRYYGVADYYTVD
/translation="MITLAVRLAULAFILIAVLALSFLGIRYADLGRYYGVADTAVVAG
UHLPRTGGLFTHSDVTYRGVSVGRVGPIDLTAEGVVAELRIKKSAPRIPADTKAVVAG
USAVGBQYIDLRPESDGSPYLADGTRIKADADTEVPADPYTDVLTSVDDLASSVPLEDLR
TVVDEFGKAPDGHGDLQVLLDSGSDFVEAADRALPSTTLLINDGETVLRTQAQEAR
IRDFAVGAKDLAAALKGSDADLRRLLAVTPEAATQVGGLLRDLDPSLGVVLANLLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis hypothetical 46.7 kDa protein MTV051.09, aa; fasta scores: opt: 529 z-score: 488.9 E(): 1e-19; 31.3% identity in 438 aa overlap. Contains Pfam match entry PF02470 mce. Also contains possible N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="cosmid 8A2"
complement(1. .126)
/gene="SC8A2.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVAVTRORGIEELLVKYPAAVSAGATAVDGGKLDLGLAVTFFSPLPCTDGYGGTRYRN GLDLGTAPALNTDAACTAPASGGKNVRGSANAPKSGAVPDPATPGSLPSGGGRTTPAGGGSPARDGSTALPGALALPGOSSEAPAGLTGLLAPAAGGAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SC8A2.02c, possible secreted protein, len: similar to TR:053972 (EMBL:AL022073) Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SC8A2.03c, possible secreted protein, len: 413 aa; similar to TR:053971 (EMBL:ALO22073) Mycobacterium tuberculosis hypothetical 40.2 kDa protein MTV051.08, 377 aa; fasta scores: opt: 685 z-score: 681.0 E(): 2.1e-30; 36.0% identity in 311 aa overlap. Contains Fam match to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(<1.
                                                                                                                                                                                                                       DLPLPGGADLGDHPYTVTAELQDVLSLVPHSAVRVNDVAVGRITGIELGEDDWSARVT
MEINGEVRLPADATARLEQSSLLGEKYVQLVAPAKETGTGRLTDGSVIPLARTSRNTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry PF02470 mce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC8A2.03c"
/note="scax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1421. ../gene="SC8A2.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF02470 mce, , E-value 1.8e-25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/product="putati
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/note="SC8x2.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC8A2.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(123
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/product="putative secreted
/protein_id="CAC12792.1"
/db_xref="GI:10798656"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC8A2
/note="SC8A2
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           /gene="SC8A2.03c"
                                                                                                                                              STINASKDDMIADLKAVAPTLRALADAGTDLPDSLQVLLTYPFTDEVLRGVKGDYLNT
                                                                                                                                                                                                   VEEVFGALSLLLNGGGVNQLKTITRELNAALGGREPEVRSMLKRVNTLVGDLDDHRGD
                                                                                                                                                                                                                                                                             /product="putative secreted protein"
/protein_id="CAC12794.1"
/db_xref="G1:10798658"
/translation="MKRATLPRGRVAGLTAGSLAAVGLALALTLGGVSVVPSGFDGIE
                                                                                                                                                                                                                                                                                                                                                                                                                   region signal
/codon_start=1
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                                                                                     ASPLPLPSVSGAGPASGGEHG
                                                                                                                 YLSMVAVPGTEVIPPLVDGDTPGPTASATAQDGPDPAAKNPAAKNPISRKRSSGQRGS
                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                    [TDALDAVNRLSSTLATRKDDVGTVLTDLSPGLKTLERQRGSLLTMLRSLDTLSGVAV
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d="CAC12793.1"
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34.6 atcocctacggcaaccgggagctctggaggaaggttggggacggtcgtcttcatggtcccc
                                                                                 286 gccgtccaggacgggcctcagaagcttctggaactcctccaggagattgcccgctccacc 345
                                                                                                                                                            Local Similarity
                                                            GACGACCTGGCGAGCTCCGTGCCGCTGGAGGACCTGCGCACGGTCGTCGACGAGTTCGGC
                                                                                                                                             237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3699..4724)
/gene="SC8A2.05c"
/note="SC8A2.05c"
/note="SC8A2.05c, possible secreted protein, len: 351 aa;
similar to TR:053969 (EMBL:AL022073) Mycobacterium
tuberculosis hypothetical 43.7 kDa protein MTV051.06, 410
aa; fasta scores: opt: 683 z-score: 769.5 E(): 0; 33.4%
identity in 368 aa overlap. Contains Pfam match to entry
PF02470 mce. Also contains possible N-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative secreted protein"
/protein_id="CAC12796.1"
/protein_id="CAC12796.1"
/db_xref="GI:10798660"
/translation="MKRPRGKPLFKPVKERNPVAVGVAGLLVLTLVALLVYNVDRLPF
GGGTTYSADFSESAGLDEGDEVRIAGVKVGQVTGVALDGAKVKVSFEVEDAWIGDRTT
AAIAIKTVLGDKYLALDPLGSGRQDBGARIPLARTTSBYDVTQAFQDLSGTVDDIDTG
                                                                                                                                                                                                               complement(4721.
/gene="SC8A2.06c"
                                                                                                                                                                                                                                                    /note="Pfam match to entry PF02470 mce,
E-value 6.7e-30"
                                                                                                                                                                                                                                                                                                                                                                                                 RLAESFETISDTFKDSPPHVRKAATGLSDLSKSISKRDAKLSELLKGSARFTKTLENN
KSSFETLIEDGGPLLGELRDRRTAINALLKGSQDLGTELGGLVKDNEKQLGPTLKALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal peptide sequence*
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2667. .2671)
/gene="SC8A2.04c"
complement(3238. .3654)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis hypothetical 44.4 kDa protein MTV051.07, 42: aa; fasta scores: opt: 596 z-score: 625.4 E(): 2.6e-27; 33.1% identity in 320 aa overlap. Contains Pfam match to entry PF02470 mee. Also contains possible N-terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                                          complement(4254. .4670)
/gene="SC8A2.05c"
                                                                                                                                                                                                                                                                                                                                                                RVTSVLEKNNTRLGETLALVGPYYRLVGNTLGNGRWFDSYLCGVVPRDYLPETSQPST
GCLPPKQPAAAQGSGAR"
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/gene="SC8A2.05c"
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RTGADNLDGNGEAIGDGVEQFGKAAKTLDGSSGDLFETLSSLQTFTTMLKNKDTDVRT
AQERLDEVVSFFADIKDDLTGALEELGKALGQVKTFIEDNRGELKKNVDRLVPITRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:10798659"
/translation="WTRRRKIITGVLALVVLAAGGLAAARALGPGGTRVTAYFDRAIG
VYAGSDLRILGVRVGEVESVDDEGTRVRVGLRLDDGIKVPEDARAVVVA,PSVVA,DRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SC8A2.04c, possible secreted protein, len:
similar to TR:053970 (EMBL:AL022073) Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SC8A2.04c"
/note="nof--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC8A2.04c"
/note="SC8A2.04c"
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complement(2659.
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                                                                                                                                                                                                                                                                                                                             /gene="SC8A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry
E-value 3.6e-27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative secreted protein"
/protein_id="CAC12795.1"
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                                                                                                                                                         5.1%;
46.7%;
                                                                                                                                     Score 52.6; DE Pred. No. 5.5; 0; Mismatches
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                                                                                                                                       264;
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                                                                                                                                                                                                                                                                     score 112.80,
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                                  by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre
available on the World Wide Web.
                                                                                                                Notes:
                                                                                                                                                                                                                              Direct Submission
                     (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
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                                                                                            Submitted (30-NOV-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA B-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                    3 (bases 1 to 34983)
Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dehydrogenase/reductase; glucose-1-phosphate adenylyltransferase; glycosyl transferase; hydrolase; integral membrane protein; laci-family transcriptional regulator; lysR-family transcriptional regulator; oxidoreductase; reductase; secreted protein; solute-binding protein; transport system permease protein;
                                                              Colney, Norwich, Norfolk NR4
                                                                                                                                                                                                                                                                                                                      Oliver, K. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34983 bp
Streptomyces coelicolor cosmid M
AL133278
Streptomyces coelicolor sequencing at
                                                                                                                                                                                                                                                                                                                                                                                                                                             A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 34983)
Redenbach, M., Kieser, H.M., Denapaite, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetyltransferase; alpha-mannosidase; dehydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL133278.1 GI:6522830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae;
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                                                                  7UH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
   The Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eichner, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces.
   is
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   funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-3bp before the initiation codon). If this cannot be identified we choose the mo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequenced clone. It may be overlapping sections once,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4758-4778(1994)) and the FramePlot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            program of Bibb et al., Gene 30:157-66(1984) as implemented at
http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overlap between neighbouring submissions
                         /note="SCM11.02, possible integral membrane protein, len: 470 aa; similar to TR:P96418 (EMBL:292669) Mycobacterium tuberculosis hypothetical 54.8 kp. mTCY08D5.31c, 482 aa; fasta scores: opt: 2112 z-score: 2527.5 E(): 0; 61.9% identity in 472 aa overlap and to TR:069633 (EMBL:AL022121) Mycobacterium tuberculosis putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SCM11.01c, hypothetical protein, len: >587 aa; similar to various hypothetical proteins, e.g. TR:092BJ0 (EMBL:AL035161) Streptomyces coelicolor conserved hypothetical protein SC9C7.20, 860 aa; fasta scores: opt: 588 z-score: 654.5 E(): 4.4e-29; 30.4% identity in 542 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLRWTHTQGYIRRDETGRPRRIIGIVRDATQEMADIAASREQAALDEARRRLTNVVQL
ATAALAHARTVDDVLDVLRDTHGLTRLGATSLVMGLVEAGRIRLVADGPENSFIPGTR
VTRIDEPYPMSEAVRTLSPRFESPEEFAERVFGLMKDITHLDITAAAYLPLIAQARP
                                                                                                                                                                                                                                                                                     /gene="SCM11.02"
1887. .3299
                                                                                                                                                                                                                                                                                                                                                        /gene="SCM11.01c"
1874. .1879
1887. .3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRVQQHVSPGDPEGLTEARHMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVPGCDVAVRYRAASIGGALGRDIGGDWYDLIPLPGGRVGAVIGDVQGHDTHAAAVM
GQLRIVLRAYAAEGHPPATVMARASVFLHELDTDRFATCLYAEADLGTGVVQVVRAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein SCM11.01c"
/protein_id="CAB61912.1"
/db_xref="GI:6522831"
                                                                                                                                                                          /gene="SCM11.02"
/note="SCM11.02, po
470 aa; similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {	t GADLDEGMDVLTALITSGPQDVRDLADRLIDVVDERRGDDDVALLVLRRHGLGAPRTF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAHEVFDLRPEEYDGRPESLALRVPTAESRRMDTIVARAMKDGSENYGTYFRLRRRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1. .1764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {	t IDPLLRFGDGTCRLVRVEGGLPLGLSAEFGRLAYPVATLELDPGNTLLLCTDGLVEQP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGAIGLLYSDRHGFSPEDRNVLVALGSGIAQSLQRAMLYEQEMDLAEGLQQAMLPRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSDRGASAPSLPDDWPAHPDPILALNRMGSFDWDLDAGLFHMDA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Streptomyces
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:100226"
/clone="cosmid M11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="nominal overlap with Streptomyces colicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "SCM11.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or longer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coelicolor A3(2)"
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scores: opt: 122
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CDS gene

SAQ IDAWLERMLAACEEGAPGRMHLHAEYDATWYQDDQPFTPAQAARQGAVTAVHSWV FNOTAQRHGRTSVPSEHHAAYLIELSKAWADDPHRPVWLQEVGAPAPLVPAEHAAAFT

CDS

FEATURES

gene

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//UD_ASET OR CONTROLING AS THE PROBLY PESYPLDVAVWNAPGEPVP //ITAINSIATION. WHIDDRSLYEARLKRYLDERVPPALYPESYPLDVAVWNAPGEPVP //ITAINSIATION. WHIDDRSLYEARLKRYLDERVPPEWAGKTVEAILDLGFDENWPGFQ CEGLVYREDGTPVKGLWPRNQWYRIGAPVEGEDVLLYEAASNPVILDYHPFWPTRL GDWDASSEPQYTLTERWDLAVLDETWNLVLDLEVLGELMAELPUSSPRWEILIANVD KALDAIDLQDVNGTAEQARSRLTEVLAAPAVPSAHRISAVGHAHIDSAWLWPLRETVR KVARTTSNWTALLEDEPDFVFAMSQAQQWAWWRDHREPWARKVKAVADGRFYPAGGK KVARTTSNWTALLEDEPDFVFAMSGAGQWAWWRDHREPWARKVKAVADGRFYPAGGK KVARTTSNWTALLEDEPDFVFAMSGAQQWAWWRDDTFGFAAGLPQIIKAAGAK YLLTQKISWSQTNKFPHHTFRWGIIDGTRIFTHEPPVDTYNCSMKGSEIAHAATNFKD KYLLTQKISWSQTNKFPHHTFRWGIIDGTRIFTHEPPVDTYNCSMKGSEIAHAATNFKD KYLTQKISWSQTNKFPHHTFRWGIIDGTRIFTHEPPVDTYNCSMKGSEIAHAATNFKD KYLTQKISWSQTNKFPHHTFRWGIIDGTRIFTHEPPVDTYNCSMGARALAGEDDTPLVFNWGELYLLHRATIJSQAKTKQGNRFSEHLLREAELWAATAAVRAGFPYPDDLD RIWKTYLLHQFHIDILFOSSIAWYHREARATYDRVAAELNGIIDAAQRALAGEDDTPLVFNSAPHARAGYPAGAAASPATDGRTGLSPRGGGHVLDNGLLRVEIDERGLVVSAYDL AADRETIAPGGAGNILLQLHPDFPNMWDAWDYAGFTKRTTTDLTDADEVVPGDDGASVR
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aa; similar to TR:AAC00190 (EMBL:AF044414) Homo sapiens
alpha-mannosidase 6A8B, 1062 aa; fasta scores: opt: 1326
z-score: 1446.5 E(): 0; 37.8% identity in 1013 aa overlap
and to SW:MANI_RAT (EMBL:M57547) Rattus norvegicus
alpha-mannosidase (EC 3.2.1.24), 1040 aa; fasta scores:
opt: 185 z-score: 1401.8 E(): 0; 35.9% identity in 1041
/translation="mpsavrfgvnytpsvgwfhhwldfdldsvradldsiaaldvdhy
RVfplwpyfqpnrtlireravedlvalvdaagergldvnvdglqghlssfdyvpawtr
TWHRRNLfTDPDVVEGQaaylrtlaaalagrpnflgwtlgnevnqfsagphpdpdrat
                                                                                                                                                                                                                                                                                                                             Complement(6484...7731)

/gene="SCM11.04c"
/gene="SCM11.04c"
/note="SCM11.04c, hypothetical protein, len: 415 aa;
similar to TR:CAB56687 (EMBL:AL121596) Streptomyces
coelicolor hypothetical 71.4 kD protein SCF51A.35, 644 aa;
fasta scores: opt: 205 z-score: 234.7 E(): 1.1e-05; 26.0%
identity in 408 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(6350..6353)
complement(6484..7731)
/gene="SCM11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVRSFGSSRVTQVLTLAPGERRLEVDTEVDWHETEKFLKLAFPLDVHAERYASETOFG
HFHRPTHTNTSWEAAKFEACNHRFVHLEEPGWGVALVNDSTYGHDVTRTVRTDADAGT
TTTVKLSLLRAPRFPDPETDQGVHRFRHALVPGAGIGDAVREGWRINLPERHLTGGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEMFTAPDYWLARLYFQRALAVVYLVAFLTAALQFRALLGERGL
TPVPREVERVPFRRAPSLFQWRYSDRLFAGCAWAGCAVSAALAAGLDALLPLWGAMLL
TPVPREVERVPFRRAPSLFQWRYSDRLFAGCAWAGCAVSAALAAGLDALLPLWGLHFR
WLVPWALYLSIVNVGQTWYSFGWESLLLETGFVAVFLGNEEVAPPVVVLFLLEWLLFR
VEFGAGLIKMRGDECWRKLTGLDHHHETQPMPGPLSWFFHHLPKPLHRVEVAANHVTQ
LVVPFLLFAPHPVSTAAALMIATQLWLVLSGNESWLWWYTIYLALSVYRFFPADAPSV
AAAPLWYEVVVLAVAALLVFLSHRPVRNMISRRQVMNRSFDSLHLVNTYGAFGSVSRV
AAAPLWYEVVVLAVAALLVFLSHRPVRNMISRRQVMNRSFDSLHLVNTYGAFGSVSRV
                                                                                                                /product="hypothetical
/protein_id="CAB61915.1
/db_xref="GI:6522834"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative alpha-mannosidase"
/protein_id="CAB61914.1"
/db_xref="GI:6522833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3319. .6342)
/gene="SCM11.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              z-score: 149.8 E(): 0.58; 27.7% identity in 166 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LERPLADTEAPRPDGDRIAVSLRPFQLTTLRLKRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVAPLVTVDRDAVVVTAVKLADDGSGDVVVRFHEAHGGRTRATLTAGFAVADVQVTDL
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complemen+/?~~
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/protein_id="CAB61913.1"
/db_xref="GI:6522832"
                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {f YAGSWFGTFVERLLENDRATLKLLRSSPFPPDAPPRFVRARLFRYRYTTWRELRETGA}
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                                                                                                                                                   915.1"
                                                                                                                                                                                                            SCM11.04c"
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JOURNAL
MEDLINE
REFERENCE
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ORGANISM
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SC4A10/c
                             REFERENCE
                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                     AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 157;
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Best Local Similarity
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AUTHORS
                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                        AUTHORS
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RSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 gcccgctccaccatcccctacggcaaccgggagctctggaggaaggtggggacggtcgtc 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 ttcatggtccccctggagatgttggccctcaacctgggggtcacccggcagaccgtccac 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aacggcgtgctctccttcaactgggtcaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcctggaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttcaccaaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gccaggctcaccctggacgactacatctacccctggaggaacctcgccctagacatggcc 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtcaacggggagcgccgggccatcggcaccctttgggccgtccggctgaggccagggaaa 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCAAGCCGGACCCCGACCCGAGTGCCCTGCTCGTCACCCTCGACCAGCCCGTCGTC 21578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCAGTCCACCGGCCGCACCCTCAAGCTGGACTTCGCGAGCCCGCTGGCCGCACCCCCG 21698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCACCGACACCGAAGGCAACGTTGTCAACGCCTTCTGGAGCAGCGGCGGCAACGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carotenoid dehydrogenase; cell division protein; DNA-binding protein; fts1; fts0; ftsW; ftsZ; isoleucyl-tkNA synthetase; lipoprotein signal peptidase; metry lenettrahydrofolate reductase; methyltransferase; murb; murE; murF; murG; murX; Na+antiporter; peptidoglycan biosynthesis; pseudouridine synthase; sporulation protein; thiamin phosphate pyrophosphorylase;
                                                                                                                                                                       A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC4A10 43147 bp D
Streptomyces coelicolor cosmid 4A10.
  James, K.D.,
                                                                                   Saunders, D.C.
                                                                                                                                               9700035
                                                                                                                                                                                                                                                          Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                     Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL109663.1 GI:5689939
                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcriptional regulator.
                          (bases 1 to 43147)
                                                                                                                 (bases 1 to 43147)
                                                                                                                                                                                                                                                                                                                (bases 1 to 43147)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-protein-dependent transport systems inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-protein-dependent transport systems inner membrane component and to Prosite entry PS00402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCM11.05c, probable transport system permease
protein, len: 306 aa; similar to TR:P73854 (EMBL:D90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7763. .8683)
/gene="SCM11.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCM11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADTGHLAARGITEVVTPDQVPVP"
  Parkhill, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.18;
                                                                                      and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 174;
  Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                    Streptomyces
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JOURNAL
                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most-upstream initiation codon.

If the connot be identified we choose the most-upstream initiation codon. If the sequence we need to the sequence of the sequence of the sequence of the sequence of the course we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-1999) Streptomyces coelicolor sequencing projesanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        small overlap between neighbouring submissions. Cosmid 4A10 Lies between and overlaps with cosm the AseI-C genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strand)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     un/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="St
<1. .205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SC4A10.01, hypothetical protein, partial CDS, >67 aa; unknown function, probable CDS suggested by frameplot and positional base preference. Continues cosmid 4G6 as SC4G6.39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Streptomyces
/strain="A3(2)"
/db_xref="taxon:100226"
                                   /note="SC4A10.02c, hypothetical protein, len: 196 aa; unknown function, probable CDS suggested by GC framep positional base preference and amino acid composition Annotated in cosmid 466 as SC4G6.38c"
                                                                                                                                                                          /gene="SC4A10.02c"
complement/100
                                                                                                                                                                                                                                     complement(190.
                                                                                                                                                                                                                                                                SEWTRSYRTRSGTORVERVYSPA"
                                                                                                                                                                                                                                                                                                                         /product="hypothetical
/protein_id="CAB51977...
/db_xref="GI:5689940"
                                Annotated in cosmid 4G6
                                                                                                                 /gene="SC4A10.02c"
/note="SC4A10.02c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="overlap with Streptomyces coelicolor cosmid 4G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC4A10.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               /label=SC4A10.01
                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cosmid 4Al0"
                                                                                                                                                                                                                                                                                                 translation="IRAANRHVRWVDTDRHGYGVLDITADRAQMDYYVVSDRTDPRAT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SC4A10.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "SC4A10.01"
                                                                                                                                                                                                                                                                                                                                                       7.1"
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                                                                                                  frameplot,
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/transl_table=11

CDS

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/note="SC4A10.03, possible membrane protein, len: 382 aa; unknown function, shows weak similarity to parts of many hypothetical proteins e.g. Sw:YB83_METJA (EMBL:167556) Methanococcus jannaschii hypothetical protein (361 aa), fasta scores; opt: 222 z-score: 255.3 E(): 6.7e-07, 24.8% identity in 306 aa overlap. Contains hydrophobic, possible membrane-spanning regions. Contains Pfam match to entry pr00924 UPF0003, Uncharacterized protein family UPF0003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2056. 3642)

/gene="SC4A10.04c"
/gene="SC4A10.04c"
/note="SC4A10.04c, possible Na+/H+ antiporter, len: 528
/note="SC4A10.04c, possible Na+/H+ antiporter of
aa; shows weak similarity to the N-terminal portion of
eukaryotic Na+/H+ antiporters e.g. SW:NAH3_RAT
(EMBL:M85300) Rattus norvegicus sodium/hydrogen exchanger
3 (831 aa), fasta scores; opt: 271 z-score: 293.1 E():
5.3e-09, 25.8% identity in 481 aa overlap. Similar to many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Na(+)/H(+) exchanger (542 aa) (31.4% identity in 528 acoverlap). Shows weak similarity to SC6673.14c (EMBL:ALO/9348) S.coelicolor probable Na(+)/H(+) antiporter (514 aa) (27.5% identity in 545 aa overlap)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="METILRPLIVVGGSVLLTVVIGWATDLLLRKADGRHPETPLWGL
LRRARVPYQIVUCSGLLRGSVYEAGVFFEHRTGYGTLTLLLIGAMLTVTRIAAAV
ETSYSSRYAHAHAERDPARVRRVRTQVSLLMRVVTAVVGVVAVSSMLLTFPAMRAAGAS
LLASAGIIGIVAGVAAQSTLGNLFAGFQIAFGDMVRMGDTVVVDGEWGTVEEITLTYL
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886. .2034
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LHGTSDLAPNASVDELPVQLHVAEPDPFETDDWLSAWYLQMGRIGADVEVHRYPGAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains hydrophobic, possible membrane-spanning regions. Contains Pfam match to entry PF00999 Na_H_Exchanger, Sodium/hydrogen exchanger family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative Na+/H+ antiporters e.g. SW:YU23_MYCTU (EMBL:277163) Mycobacterium tuberculosis putative
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complement/por/
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/note="Pfam match to entry pF00924 UPF0003,
/note="Pfam match to entry pF00924, Score 15.70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVRTWDERRITMPVSYFTSKPFENWSRGTPQMTGTVFWHLDHSAPMDLMRERLRDILR
ECPAWDGRNYNLTVTDTTPTTMEVRALVTAKDADDIWTVRVTVREGMLRWLADEHPYA
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/protein_id="CAB51978.
/db_xref="GI:5689941"
                                   DEDIPTSWRETVVMWAGMRGVASVALALAIPLETDDGAAFPHREEIVFIAFGVIMGT
LLLQGLTLPWLVGRLGVRADTEREQEFERDLALRAAKAAKQRLKEIESVEELPEELSE
                                                                                                                                               VPNVDIPPELIIPGLLPPLLYAÄVRRTSWRQFAANKRPIFLLAVALVEVTMVCVASVA
HAIVFGLPIAAAFALGALVAPPDPVAATAVAGGLGLPRRLVSILEGEGLENDVTAIVL
YHVAIAAAVGGSESPWRAGGDLVLSAVVAVAIGLTVLGWSGNKLMSVLGDPPLQIGLTL
LVPFVSYVAADELHGSGVLAVLTTAMFLAEYASDADDVMTRLGGHTVWDVVDTLVTGV
                                                                                                                                                                                                                                                                                                                                      /product="putative Na+/H+ antiporter"
/protein_id="CAB51980.1"
/db_xref="GI:5689943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPRVNTADAALRPPRAGLPHARHAPDPAAGRSSDGDARRFPGRPAKSL"
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/protein_id="CAB51979.1"
/db_xref="GI:5689942"
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{	t QMLRRAFDIGIRISPDLGDEERREAQEQRARRIKRVRRIQGEMLSAARHEVLAARSEP}
                                                                                                               AFGLIGLELHNAVRTASGRWTELLGWAAAILVVVVLVRLLWLLPATWLTQRLHARRDQ
                                                                                                                                                                                                                                                                                                          translation="MDQLALLFMLLLGALLSVPIGARLGLPAPVLMTLLGIVLALLDF"/
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                                                                                                                                                                                                                                                                                                                                                         CGCGGCCCAGGAGGGTGTGGACTACTTCTGCACCGGCCCGTGCTGGCCGACCCCCACCAA 42289
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                                       complete
AF357202
                                                                            Streptomyces nodosus amphotericin
                    AF357202.1
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/note="SC4Al0.05c, hypothetical protein, len: 160 aa;
unknown function, shows weak similarity to hypothetical
proteins from other eubacteria e.g. SW:YYBD_BACSU
(EMBL.D26185) Bacillus subtilis hypothetical protein (147
aa), fasta scores; opt: 199 z-score: 236.4 E(): 7.6e-06,
36.8% identity in 144 aa overlap. Shows weak similarity to
SC5F7.12c (EMBL.AL0.96872) S.coelicolor possible
acetyltransferase (169 aa) (37.7% identity in 114 aa
overlap). Contains Pfam match to entry PF00583
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/note="sc4"
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/db_xref="GI:5689944"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC4A10.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MPSRAPAAYEVRVAEDPVDREACFAVRKDVFVAEQKVPEDIEYD/
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/transl_table=11
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6;
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JOURNAL REFERENCE
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Caffrey,P., Lynch,S.V., Flood,E.M., Finnan,S.M. and Oliynyk,M. The amphotericin biosynthetic gene cluster from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces nodosus Streptomyces nodosus Bacteria; Firmicutes;
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Caffrey, P., Lynch, S.V.,
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FVAAPLMCLGSVLLALRQDVTLALILVPMVLVVAVCFGLLLSRWAALXARLQOTLDRI
GRLLRRITGVRVVRSFARDAHEGERFTRTNEELLGLSLGVGRLIAVMLPSVLLLMNL
FTLGLLWYGAARRIDSGSMQIGALSAFISYLSLILMSVVMLAFVFLNVPRARVCAERIT
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                                                                                                                                                                                                 transl_table=11
                                                                                                                                                                                                                                                        note="mycosamine biosynthesis protein"
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                                                                                                                                                                      LDDLLLAHSW"
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                                                                                                                                                                                tggggacggtcgtcttcatggtccccctggagatgttggccctcaacctgggggtcaccc 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, EP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottler,F., Camus,J.C., Cattolico,L., Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Giguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.

Genome, sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia solanacearum.
Ralstonia solanacearum
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INRA, BP27, F31326 Castanet-Tolosan Cedex
Christian.Boucher@toulouse.inra.fr
http://sequence.toulouse.inra.fr/R.solanacearum.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, Fran Laboratoire de Biometrie et Intelligence Artificielle INRA,
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AL646072 AL646052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:17429824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solanacearum'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome,
                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical
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                                                                                                                                                                                                                                                                      PROTEIN'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence;
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(SMALL CHAIN) OXIDOREDUCTASE PROTEIN"

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predicted by Homology
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Gene name confidence : putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGALSWD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNAPMFKGYLRFICNRRCQQIGLDALFPNEDNPFPWMSEMIDLKKERNFFETRVIEYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="nrdB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     name
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d by Homology
d by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RS00300"
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140097 CTTCCTCATCCCGGAACTGGTCAGCGGCATCGCCTACAAGAAAGGCACCTACTTCGCAGA 140156

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Š

387

Matches Query Match Best Local

187;

Conservative

0

198;

6

Gaps

Similarity

5.1%; 47.8%;

Score 52.2; Pred. No. 4; Mismatches

DB 1;

Length 188050; Indels

Db 140037

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complement (7472. 9184)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="RSc2807; RS00298 complement(7472. .9184)
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predicted by Homology
predicted by FrameD"
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regulator protein"
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HSV-2 strain SB5 C
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ND BIOLABS	98US-0134246	98US-0134246			ocation 1026 *tag= product codon=		in; RepT; nce gene; n; ds.	on protein,	st entry)		DNA;		44377 492 492	44377	2562	066 066	58857 4097	2584 2584	897 1314	77536	2614 2614 24379	35026 65140	131 4 12588	4451	1833	4767 2458	1290	1620 .2668 .1686
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							s plasmid; i;	5 plasmid.					Platenolide syntha Human foetal liver Probe #5445 for ge		tral H	in secreted pro	Nucleotide sequenc Endothelial nitrog		Thiomonas cuprina H. vulgare nicotia	Nucleotide sequenc		la pe Yces	Bordetella pertuss Sequence encoding	hetic human Fa	Drosophila melanog Pseudomonas aerugi	ggregatum HSF1 fusio	mays DNA frac	L-1 gend L-1 gend domonas

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present DNA sequence encodes Thermus sp. replication protein, RepT CC which is obtained from pTsp45S plasmid The replication protein, RepT is needed for thermophilic plasmid replication.

CC needed for thermophilic plasmid protein protein RepT, partition the invention relates to Thermus sp. replication protein RepT, partition protein ParA and their corresponding DNA molecules which relates to recombinant DNA molecules encoding plasmid DNA replication origins in Thermus, as well as to shuttle vectors which contain the same The green which comprises inserting plasmid DNA comprising a Thermus sp. plasmid genes which comprises inserting plasmid DNA comprising a Thermus sp. plasmid of replication (Ori) into a recombinant plasmid comprising a thermostable kanamycin-resistance gene and an Escherichia coli Ori, to produce a cloned recombinant plasmid. This cloned recombinant plasmid is transformed with an E. coli host cell, and E. coli host cell cultured for the expression of cloned recombinant plasmid. The cloned recombinant plasmid isolated from E. coli host cell, so then transformed with Thermus sp. plasmid genes are cloned. These plasmid DNAs are used for thermostable transformation.
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Best Local Similarity
Matches 1026; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning Thermus species (Ts) plasmid genes comprises transforming Escherichia coli with cloned recombinant plasmid containing Ts and E.coli origins of replication, isolating cloned recombinant plasmifrom E.coli and transforming Ts cell -
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kanamycin-resistance gene;
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Cloning Thermus species (Ts) plasmid genes comprises transforming Escherichia coli with cloned recombinant plasmid containing Ts ann E.coli origins of replication, isolating cloned recombinant plasm from E.coli and transforming Ts cell

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Best Local Similarity
Matches 1026; Conserv
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The invention relates to Thermus sp. replication protein RepT, partition protein ParA and their corresponding DNA molecules which relates to recombinant DNA molecules encoding plasmid DNA replication origins in Thermus, as well as to shuttle vectors which contain the same. The invention also relates to method useful for cloning Thermus sp. plasmid genes which comprises inserting plasmid DNA comprising a Thermus sp. origin of replication (Ori) into a recombinant plasmid comprising a thermostable kanamycin-resistance gene and an Escherichia coli Ori, to reproduce a cloned recombinant plasmid to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               produce a cloned recombinant plasmid. This cloned recombinant plasmid is transformed with an E. coli host cell, and E. coli host cell cultured for the expression of cloned recombinant plasmid. The cloned recombinant plasmid isolated from E. coli host cell is then transformed with Thermus sp. host cell and Thermus sp. host cell and Thermus sp. plasmid genes are cloned. These plasmid DNAs are used for thermophilic transformation.
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                                           The sequence shown is that isolated from Thermus aquaticus genomic DNA and encodes a heat resistant super oxide dismutase enzyme. The gene is useful for medicines for inflammation and as a protection against X-rays, as a reagent for research in enzyme electrodes or an enzyme for a bioreactor.
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                                                                                                                                                                                                                                           Gene, of and plasmid contg. heat resistant super:oxide dismutase - for treating inflammation, X=ray protection, enzyme electrodes
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  Sequence
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    615 BP; 125 A; 223
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Query Match Best Local Similarity

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 Claim
                               A DNA encoding a protein with a neoxanthin cleavage activity producing transgenic plants with improved or decreased stress
                                                                                                                                                  13-JAN-2000; 2000JP-0010056.
11-JAN-2001; 2001JP-0003476.
                                                                              WPI; 2001-400081/43
                                                                                                                                                                                    11-JAN-2001; 2001EP-0300218
                                                                                                                                                                                                            18-JUL-2001.
                                                                                                                                                                                                                                   EP1116794-A2
                                                                                                                                                                                                                                                                                                                  Zea mays.
                                                                                                                                                                                                                                                                                                                                      plant growth protectant;
                                                                                                                                                                                                                                                                                                                                                Maize; neoxanthin cleavage enzyme; VP14; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD09400 standard; cDNA; 1815
                                                                                                     Iuchi S,
                                                                                                                            (RIKE )
                                                                                                                                                                                                                                                                                                                                                                                  Zea mays neoxanthin cleavage enzyme, VP14 cDNA
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Best Local Sim
Matches 177;
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                                                                                                                              HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                 Herpes
                                                                                                                                                                             HSV-2 strain SB5 Contig ID 10 DNA sequence
                                                                                                                                                                                                                                                AAV62154;
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Similarity 45.9%;
77; Conservative
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                                 complement (1..5672)
/*tag= a
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/product= "ORF#1
                                                                 Location/Qualifiers
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xcept= (pos: 1..2,
"ORF#1 protein"
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Pred. No. 0.013;
""matches 209;
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                    aa:
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                                                                                                                                                    This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 10, and encodes B HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
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P-PSDB; AAW72095, AA
AAW72101, AAW72102.
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04-NOV-1996;
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                                                                                                                21034 BP; 3154 A; 7419 C;
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Leary JJ;
                                                                                                                                                                                                                                                                                                                                                                                      350-359; 748pp; English.
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96US-0030279.
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/product= "ORT#8 protein"
/note= "encoded protein - L-
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/product= "ORF#7 protein"
/note= "encoded protein s
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/note= "encoded protein s
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                       4.78;
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unspecified amino acid"
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Score 48.6; DB 19;
Pred. No. 0.12;
0; Mismatches 264;
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/note= "encoded protein s
complement (3802..6447)
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/note= "encoded protein shown
1170...2174
/product= "ORF#6g protein"
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                                             Human herpesvirus 2; cytostatic; cancer; immunosuppressive; virucide; antibacterial; fungicide; protozoacide; antirheumatic; antiinflammatory; antiarthritic; rheumatoid arthritis; neuroprotective; multiple sclerosis; immune response; vasotropic; vaccine; gene therapy; autoimmune disease;
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                    Human herpesvirus
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The invention relates to a composition comprising an expression vector cobound to an aggregated protein-polycationic polymer conjugate or suspension. The expression vector contains a promoter polynucleotide cathigen which is a fragment of a gene or genome associated with an comprising of bacterium, fungus, protozoa and virus such as human consisting of bacterium, fungus, protozoa and virus such as human consisting of bacterium, fungus, protozoa and virus such as human consisting of bacterium, fungus, protozoa and virus such as human consisting of bacterium, fungus, protozoa and virus (HSV), hepatitis consisting of bacterium, fungus, protozoa and virus (HSV), hepatitis consisting of bacterium, fungus, protozoa and virus (HSV), and consisting a nucleotide sequence encoding a cytokine (or a cytokine expression vector), is useful for inducing an immune response contains a sequence for granulocyte macrophage-colony stimulating factor (GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding the antigen and the cytokine are under transcriptional control of same or contains a sequence is useful for treating a condition in an organism. The correspondence is human herpesvirus 2 complete DNA genome related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 90-132; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing antigenic protein-polycationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    delivery of vaccines, comprises expression vector genomic sequence, bound to aggregated polymer conjugate or suspension -
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Sequence 154746 BP; 23003 A; 54218 c; 54701 G; 22824 T; 0 other;

4.78; 43.98;

Score 48.6; Pred. No. 0.

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RESULT
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P-PSDB; AAB10432, AJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody library
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                 vector pSEX11L4 encoding protein G, used in the method of the invention
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Best Local Similarity
Matches 197; Conser
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                                                                                                                                                                                   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restencests; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
19-DEC-1997;
14-MAR-1997;
14-MAR-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
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  97US-0040710.
97US-0040762.
97US-0048100.
97US-0048189.
97US-0048357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to CC generate fusion proteins by linking to the gene to a human immunoglobulin CC Fc portion (e.g. AAV34277) for increasing the stability of the fused CC protein as compared to the human protein only.

CC rate invention relates to 28 novel genes and their fragments (nucleic CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235) CC which are useful for preventing, treating or ameliorating medical CC conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 28 CC polypeptides in a sample or by determining the presence of mutations in CC conditions, based on which tissues they are most highly expressed in CC (see AAV34286 for described uses).
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Best Local :
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06-JUN-1997;
05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1473 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 144-145; 201pp; English.
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Li H, Li Y,
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GCGGCTGAGTCCGGTACCCTCTAAGTGGCCCCTGGTAGAAGCAGTGGTCCTGCCCGCGAGG
                      atgcccaacaccaagaccgttggccgttgacctgggcctcatcctggtcctccccgaggtg
                                                                                      gaccacggaatccgccccaccctggacgtgctggtcctctgggctcaggggaaaagggtg
                                                                                                                       TGCTCAGCCTGGTACACGCCGTGCCGTCCGCCCTCGCCACCTTCATCCAGGGGCTCGATC
                                                                                                                                            aacctcgccctagacatggccaacggcgtgctctccttcaactgggtcaaggcctaccag
                                                                                                                                                                                 CCCAGGAGGCTGCCCAGGCTGTCGTCGCTGACCCCGCAGGTCCCGGCCGTCTGCAGCAGG
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DB; AAW75227.
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97US-0048970.
97US-0057765.
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Pred. No. 0.23
0; Mismatches
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Ruben S
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289 gtccaggacgggcctcagaagcttctggaactcctccaggagattgcccgctccaccatc

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Score 45.6; DB Pred. No. 0.33; 0; Mismatches

289;

Indels

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Length

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RESULT 10
AAQ224482
ID AAQ224
XX AAQ224
XX AAQ224
XX STOEL-
XX Heat s
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XX WO9204
XX WO9204
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Query Match
Best Local Similarity 43.1
Matches 219; Conservative
                                                                                                                                                                                      The sequence is that of the coding region of the groEL-1 gene which codes for the 18 kDa heat shock protein HSP18. The gene actually codes for a 56 kDa protein but this is subjected to post translation modifification to give the 18 kDa HSP18 protein.

See also AAQ22477-Q22486.
                                                                                                                                            Sequence 1620 BP;
                                                                                                                                                                                                                                                                                                                                                   Claim 18; Fig 8; 50pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA contg. heat inducible promoter gene - also vectors, transformed cells and new proteins of Streptococcus albus
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Matches 219; Conserv
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21-MAR-2000; 2000US-191078P
                                                      21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa DNA for cellular proliferation protein
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ARESULT 13
AAV62134/C
ID AAV62134 standard; I
XX
AC AAV62134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC pseudoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets of or antibiotic development. The antisense nucleic acids can also be used CC identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIPO at
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Best Local S
Matches 134
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1686 BP; 307 A; 607 C; 528 G; 244 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Seq
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DB; AAU36507.
                                                                                                               accaggaccacggaatccgcccc
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                                                                                              acggcgacaacccggtcaccgcc
                                                                                                                                                   tgagcgaccgcatcctgttcagcggcaagcgcccatcggcgtctcctacctggtgggca
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; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Xu HH;
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51.0%;
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/note= "encoded protein s
complement (6263..6745)
         /product= "ORF#15 protein"
/note= "encoded protein shown
24286..25632
                                                                                                                                                                                                                                                                                                                                     /product= "ORF#9 protein"
/note= "encoded protein shown
complement (17295..19110)
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/note= "encoded protein s
complement (8386..9477)
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/note= "encoded protein shown
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/note= "encoded protein s
complement (9721..13911)
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/note= "encoded protein s
complement (3637..6093)
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/note= "encoded |
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/product= "ORF#1 protein"
/note= "encoded protein s
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complement (256..3021)
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23778..24065
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22307..23887
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/note= "encoded p
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/note= "encoded protein s
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                                                                             /product= "ORF#14 protein"
/note= "encoded protein shown
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/note= "encoded protein sh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 104, and encodes 17 HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in
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04-NOV-1996;
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                             tgggtcaaggcctaccaggaccacggaatccgcccaccctggacgtgctggtcctctgg
           tacatctacccctggaggaacctcgccctagacatggccaacggcgtgctctccttcaac
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pathway; promoter; termination sequence; corn; ss.
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Best Local Similarity 47.2%;
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Pred. No. 0.38
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This invention describes novel DNA sequences encoding for polyketide C (PK)-like synthesis (PKS-like) pathway genes from Shewanella, Vibrio cand Schizochtrium. The nucleic acids are useful for isolating related CC molecules or in methods to detect organisms expressing the PKS-like CC genes. They are also useful for creating transgenic plants that express C poly-unsaturated long chain fatty acids. The poly-unsaturated long chain fatty acids produced recombinantly are useful as dietary supplements for CC patients undergoing intravenous feeding or for preventing or treating CC malnutrition. The poly-unsaturated long chain fatty acids can also be incorporated into cooking oils, fats or margarine formulated so that in CC normal use the recipient receives a desired amount of poly-unsaturated CC production of the fatty acids and edicated and elcosapentenoic acid, and for the CC modification of the fatty acid profile of host cells and edible plant CC tissues and/or plant parts. Transgenic production of polyunsaturated CC faity acids in particular host cells allows quicker purification from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKS pathway; polyunsaturated long chain fatty acid; plant; transgenic; polyketide-like synthesis; PUFA; dietary supplement; intravenous feedi malnutrition; cooking oil; cooking fat; margarine; docosahexenoic acid production; elcosapentenoic acid production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA sequences encoding for polyketide (PK)-like synthesis pathway genes from Shewanella, Vibrio and Schizochtrium, useful for creating transgenic plants that express poly-unsaturated long chain fatty acids
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SURVEY Sequence.

Persynta Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Pterygota; Neoptera; Pterygota;

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                           J., Oates,R. and Main,D. Development of a genetically and physically anchored for barley genomics: Morex rachis cDNA library Unpublished (2001)
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rar
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                                                                                 Contact: Wing RA
Clemson University Genomics
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                          Fax: 864 656 4293
                                        100 Jordan Hall,
Tel: 864 656 728
                                                                  Clemson University
                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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              rwing@clemson.edu
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/ob_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19116"
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); State University,
Pullman, WA in a greenhouse, the rachises were excised and
frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
lab at the University of California, Riverside total RNA
was prepared, poly(A) was purified, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
sequence has been trimmed to remove vector sequence and
contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 249 c 158 g 105 t
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/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
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/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.genome.clemson.edu/projects/barley. To order
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/lab host="TJC121"
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BM335757.1
EST.
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rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Contact: Patrick (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S
Expressed Sequence Tags from B73 Maize: various stages
including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM335757 502
MEST160-F05.T3 ISUM5-RN Zea
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 515-294-2299
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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515-294-0975
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                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPC
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                                                                                                                                                                                                                                                                             (1-aminocyclopropane-1-carboxylix acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscisc acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was
                                                  resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the
                                                                                                                                                                                                     prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="MEST160-F05"
/clone_lib="ISUM5-RN"
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/cultivar="B73"
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NotI sites of the pT7T3PAC vector. through one round of normalization
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF259495 759 bp mRNA linear EST 22-OCT-2001 HVSMEf0019H19f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0019H19f, mRNA sequence.
                                                                                                                                                                                                             Email: rwing@clemson.edu
Total hq bases = 388
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                Problems of a genetically and physically anchored EST resource Development of a genetically anstressed seedling root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
                                                                                                                                                                                                                                                                         100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                               Clemson University
                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                          On Nov 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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BF259495.2 GI:13120022
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/clone_1lb="Hordeum vulgare seedling root HVcDNA0007 (EtLolated and unstressed)" /tissue_type="Seedling root" /lab_host="TJC121"
                                                                                                                  /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
122 c 162 g 110 t 13 others
                                                                          /db_xref="taxon:4513"
/clone="HVSMEf0019H19f"
                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                              (2001)
                                                                                                                                                                                                                                                                                                           Clemson,
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Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 133;
                                                                                                                                                                                                                                                                                                             SC
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DEFINITION
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Best Local Sin
Matches 162;
                                                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 CTACCGCGACTTCGTNCTCGACCTCAACAAGGCCCTCGCCGCCGACCAGCG 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 CATCAACCGCGAGAACTACGAGCTGGGGGCTGCCGTGCATCGAGAAGGCCGGCGTGGCGCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccccaccctggacgtgctggtcctctgggctcaggggaaaagggtgatgcccaacccaa 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catggccaacggcgtgctctccttcaactgggtcaaggcctaccaggaccacggaatccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACCACGAGCGCCTCATGAAGCTCGTCAAGGTCGGCGGCCTCCTCGGCTACGACAACAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCAACCACGGCACCTTCGACTTCGTCTTCGTGGACGCCGACAAGGACAACTACCTCAA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGATCGACTTCCGCGAGGGCCCGGCCCTCCCCGTCCTGGACGCCCTCCTCGAGGACGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccaaaccgtcaacggggagcgccggggccatcggcaccctttgggccgtccggctgaggcc 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCTGGAACGGCTCCGTCGTGCTCCCCGCCGACGCCCCATGCGCAAGTACATCCGCTA
                                                                                                                                                                                                                                                                                                                                                                                      AV436476 Porphyra yezoensis TU-1 PS002f12_r 5', mRNA sequence.
Nikaido, I.,
                                                                                                                               Eukaryota; Rhodophyta;
                                                                                           Porphyra.
                                                                                                                                                                                                                          Porphyra yezoensis.
                                                                                                                                                                                                                                                                                                                 AV436476.1 GI:8591701
                                                                                                                                                                                                                                                                                                                                                               AV436476
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                                             (bases 1 to 524)
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Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
282 c 184 g 133 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To ore this clone see http://www.genome.clemson.edu/orders /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: lambdaZAP; Site_1: ECOR1; Site_2: Xho1;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with water, nystatin and cefotaxime in covered
Asamizu, E.,
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Pred. No. 1.4;
                                                                                                                               Bangiophyceae;
    Nakajima, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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    Nakamura,Y.,
                                                                                                                               Bangiales; Bangiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The First Laboratory for Plant
Kazusa DNA Research Institute
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                         Zea mays
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
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/note="Vector: pBluescriptII SK-; Site_1:
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/clone="PS002f12_r"
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Pred. No. 2.3;
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855 California Ave,
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Contact: Walbot V
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                                                                                                                         BM332294
MEST154-H06.T3
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//lab_host="E. coli XLOLR"
//note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoR1; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."

79 a 132 c 175 g 77 t
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/cultivar="W64A"
/db_xref="taxon:4577"
/clone_lib="949 - Juver
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48.9%;
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FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)
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Contact: Patrick S. Schnable
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1 (bases 1 to 539)
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Agronomy, Iowa State University, Ames,
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//note-"Vector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
//note-"Vector: pT7873PAC; Site_1: Site_2: NotI;
//note-"Vector: pT773PAC; Site_1: Site_2: NotI;
//note-"Vector: pT773PAC; Site_1: Site_2: NAG), Kernels
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                  resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
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/cultivar="B73"
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/lab_host="DH10B"
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/clone_lib="ISUM5-RN"
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Query Match Best Local Similarity

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REFERENCE
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Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
Unpublished (2001)
                                                                                                                                                                                                                                                             BACKWARD: Backward PCR primer sequence, primer T3
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515-294-0975
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                                                                                                                                                                                                                                                                          CNS017SY 1101 bp DNA linear GSS 26 Drosophila melanogaster genome survey sequence SP6 end of BACN37L08 of DrosBAC library from Drosophila melanogaster
                                                                                               Drosophila 
Eukaryota;
                                                                                                                                                                                                                          fly), genomic survey sequence. AL108460
                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope
                                                                                                                                                                                                     AL108460.1
                                                                                                                                                     fruit fly.
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                       (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings
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Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
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Pred. No. 2.9;
0; Mismatches 134;
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Matches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fi
                Onpublished (1996)
Contact: Marra M/Mouse EST Project
Washin-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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497 bp mRNA linear EST 23-vc24h07.r1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAGE:775549 5' similar to SW:MRPLHUMAN P33527 MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1. ;, mRNA sequence.
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                                                                                          Waterston, R.
The WashU-HHMI Mouse EST Project
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Forest Park Parkway, Box 8501, St.
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/note="end : SP6"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 591)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
                                                                                                                                                                     BI960325 591 bp mrNA linear EST 22-OCT-200 HVSMEn0024D19f Hordeum vulgare rachis EST library HVcDNA0015 (normal) Hordeum vulgare cDNA clone HVSMEn0024D19f, mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                         barley.
                                                                                                                                             BI960325.1 GI:16311580
                                                                                         Hordeum vulgare
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Location/Qualifiers
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150 c
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/dev_stage="11.5dpc"
/lab_host="DH10B"
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/clone="IMAGE:775549"
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/strain="C57BL/6J"
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                                                    CGGCGGCCTCCTCGGCTACGACACCCCTCTGGAACGGCTCCGTCGTCCTCCCCCGCCGA
                                                                                              caaggeetaceaggaceaeggaateegeeeeaceetggaegtgetggteetetgggetea 719
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100 Jordan Hall, C
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Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 211 c 128 g 113 t
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/lab_host="TJC121"
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/clone="HVSMEn0024D19f"
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                                                                                      tccacgcctggaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttcacc
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945017C08.X1 945 - Mixed
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855 California Ave, Palo Alto,
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1 (bases 1 to 513)
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945017 row: C colu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
/same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
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1 (bases 1 to 534)
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Fax: 650 725 8221
Email: walbot@stanford.edu
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/db_xref="taxon:4577"
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Vector: pGAD10; Site_1: EcoRI; cDNA library from fully 
differentiated maize tissues from a active Mutator 
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk, 
husk, root, leaf). Unidirectionally cloned."
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/dev_stage="adult"
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AUTHORS
TITLE
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Best Local Similarity
Matches 132; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 GGGCGTGCAGCTCATCAACGTCGACATCAAGTACAACAGGTCCGACAACAAGACCATGTC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696 ggacgtgctggtcctctgggctcaggggaaaagggtgatgcccaacaccaagaccgtggc 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 CGGCACCTCCAACACGCCGGAGGCCATCACGCTCAACTGCGCCAACAACCTGCCCTGCCA 352
                                                                                    195
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                                                                                                                                                                                           329 agattgoccgctccaccatcccctacggcaaccgggagctctggaggaaggtggggacgg 388
                                                                                                         tcgtcttcatggtccccctggagatgttggccctcaacctgggggtcacccggcagaccg 448
                         tecaegeetggaagaaggteettgagaaaaagggeetggtggeeaeegaegteetteaee 508
                                                                                  ACGAGTACGGCATCAGGTTCAACATGCCGAGCCAGCACATCGTCATCCGGAGGCTGACCT 254
GCGTCTCCCCCACGAGCGCCATGATCGCGCTGGGCAGCGAGATGTCCGGCGGCGGCATCCGCG 314
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Zea mays
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548 bp mRNA linear EST 30-MAY-2000 945017C08.X2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Lea mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 548)
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Plate: 945017 row: C colum
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Walbot V
Department of Bilogical Sciences
Stanford University
Palo Alto, CA 94304, USA
Tel: 650 723 8221
Fax: 650 725 8221
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Maize ESTs from various cDNA libraries sequenced at Stanford University
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                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                    4.5%;
ilarity 48.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                          /note="organ: tassel, kernal, silk, husk, root, leaf; 
/ector: pGAD10; Site_1: EcoRI; cDNA library from fully 
differentiated malze tissues from an active Mutator plant. 
Tissue ratio is 4:2:1:1:11 (tassel, kernel, silk, husk, 
root, leaf). Unidirectionally cloned. New library number 
given to library 707 for additional sequencing." 
a 184 c 162 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                    0;
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Pred. No. 5.7;
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